REMARKS/ARGUMENTS

Upon entry of this response comprising amendments, claims 19, 49-51, 61-62, and 64-65 are pending. The limitations of claims 63 and 66 have been incorporated into their respective independent base claim, and thus have been cancelled.

Applicants respectfully direct the Examiners attention to the third supplemental Information Disclosure Statement filed concurrently herewith, that makes the PCT Written Opinion and newly presented reference to Kohler et al. (U.S. Patent Serial No. 5,523,208) of official record in the present application.

Applicants acknowledge the Examiners objection to an embedded hyperlink reference and have amended paragraphs 0051, and 0052 to remove the hyperlink references. Applicants have also amended the title and adopted the Examiners suggestion that Applicants assert is more descriptive of the invention to which the claims are directed.

Applicants have also amended claims 19, and 49 to replace the term "related" with "correlated" the support for which may be found in claims 19 and 49 as originally filed. Applicants have amended claims 19 and 49 to replace to term "first set" with "query comprising a user selection" (support may be found in paragraphs 0071 and 0084; and claims 19 and 49 as originally filed with respect to "a user selection"); and added the limitation of "selected from the results of one or more experiments performed using biological probe arrays" (support may be found in paragraph 0055). Further, Applicants have replaced the limitation of "a first set of one or more data" with "gene or EST data" (support may be found in

paragraph 0086) and replaced the limitation "second set of one or more data" with "a set of protein data" (support may be found in paragraph 0089 and 0090).

Applicants have additionally amended claims 19 and 49 to move the limitation of "is capable of the identification of a biological molecule" from the body of the claim to the preamble to provide antecedent basis for the probe-set limitation in the body of the claim. Similarly, the limitation of "has one or more identifiers" has been moved and reworded from the preamble to the body of the claims.

Applicants assert that no new matter is presented by these amendments and respectfully request entry of the same.

Reply to Claim Rejections – 35 U.S.C. §101

Claims 19, 49-51, and 61-65 are rejected under 35 U.S.C. §101 as being directed to non-statutory subject matter.

Applicants have amended claims 19, and 49 to include the limitation of a user selection that identifies probe-sets selected from the results of one or more experiments performed using biological probe arrays. Applicants respectfully assert that claims 19 and 49 as amended meet the requirements of 35 USC §101 under the safe harbor provisions described in MPEP §2106 (IV)(B)(2)(b)(i) that include a transformation performed outside of a computer, in particular a pre-computer process activity (i.e. a user selection, and the one more experiments performed using biological probe arrays producing results from which the selection is made) where those acts are independent of the following method

steps. Further, Applicants assert that the claimed invention causes a transformation of the selected probe set identifiers in the process when they are correlated to gene or EST data, and further transformed when the gene or EST data are correlated to a set of protein data. The protein data of claimed invention has real world value to a user such as, for instance, for the analysis of experimental results that may provide the user necessary information to determine biological significance. Additionally, Applicants assert that claims 19 and 49 as amended are not restricted to the manipulation of numbers, abstract concepts or ideas, or signals. Rather each of claims 19 and 49 claim a user selection that is not a mathematical operation or a manipulation of abstract ideas, and further that the user selection identifies probe-sets selected from the results of one or more experiments performed using biological probe arrays that similarly are not mathematical operations or manipulations of abstract ideas.

Therefore, Applicants respectfully assert that each of claims 19 and 49 are directed to statutory subject matter and comply with 35 U.S.C. §101 as well as compliance with MPEP §2106 and are thus patentable. Additionally, Applicants assert that each of claims 50-51, 61-62, and 64-65 each depend from either claim 19 or 49 and are thus also patentable for the same reasons.

Reply to Claim Rejections – 35 U.S.C. §112

Claims 19, 49-51, and 61-66 are rejected under 35 U.S.C. §112 as being indefinite.

Applicants have amended claims 19 and 49 to replace the phrase "related to" with "correlated to" with respect to providing information that Applicants assert clearly points out the subject matter of the claim. Similarly, claims 51, and 65 have been amended to include the phrase "comprising" with respect to protein family data.

Additionally, Applicants have amended claim 49 to remove the phrase "associated with" and clarify the relationship between the probe-set identifiers and probe-sets that particularly points out the subject matter of the claim. For example, the relationship includes each of the probe-set identifiers identifying one or more of the probe sets.

Therefore, Applicants respectfully assert that each of claims 19, 49, 51, and 65 as amended particularly points and out and distinctly claims the subject matter of the invention, and are thus patentable. Additionally, Applicants assert that each of claims 50-51, 61-62, and 64-65 each depend from either claim 19 or 49 and are thus also patentable for the same reasons.

Reply to Claim Rejections – 35 U.S.C. §102(e)

Claims 19, 49-51, and 61-66 are rejected under 35 U.S.C. §102(e) as being anticipated by Maslyn et al. (US Patent Serial No. 6,408,308). Maslyn et al. is generally directed to a system for processing and storing normalized biomolecular data from microarray experiments that is different than the claimed system for providing protein information correlated to one or more probe-set identifiers.

In particular, Masyln describes processing data employing a biomolecular expression information processing system (col. 10, line 34 *et seq.*) that analyses datasets of raw expression data from a microarray (col. 9, line 19 *et seq.*) and determines a summarized and normalized intensity value for the elements associated with the microarray that is stored as an abundance dataset. Generally, the Maslyn process calculates a numerical factor so that the experiments from different microarrays can be compared. This process is different than the claimed method of receiving a query that comprises a user selection of probe-set identifiers, and correlating each of the probe-set identifiers with gene or EST data.

For example, Maslyn describes generating raw expression data 140 for each element 142 (col. 5, line 23 et seq.) and a client system that receives the raw expression data 140 from the reader/analyzer 132 for processing (Figure 4B; and col. 5, line 60 *et seq.*).

Maslyn then describes microarray design information (col. 2, line 20 *et seq.*) as well as more specific microarray layout data (Figure 4B; col. 6, line 22 *et seq.)* as employed in the processing steps of summarization and abundance determination (Figure 4B, col. 6, line 18 *et seq.*). In particular, the microarray layout data is employed to correlate the elements of the microarray for computing an average intensity value for each element from the raw data, and subsequent generation of normalized abundance data (col. 6, line 33 *et seq.*) that includes a computation of relative intensity of each of the elements. Applicants respectfully assert that the description microarray layout data and how microarray layout data is employed is different than a query received that includes a user selection of

probe-set identifiers. Rather the microarray layout data is described as embedded in a data file that does not include a user selection, and further the microarray layout data is employed as a tool in the processing of information and computation to generate a result that is different than the claimed correlation with gene or EST data that is further correlated with protein family data. Rather the microarray layout data is described as being utilized in the computation of intensity values associated with the summarization and abundance determination procedures.

Maslyn also describes comparisons of datasets resulting from the processing methods described above. However, Maslyn does not describe or suggest a dataset that comprises a user selection of probe-set identifiers, or as a set of data resulting from a correlation with such a user selection.

In particular, Maslyn describes comparisons between abundance datasets (col. 10, line 47 *et seq.*) that states:

> "In particular, the system has a dataset comparison procedure 220 (FIG. 4B) that selects one abundance dataset as a base expression dataset, selects another abundance dataset as a comparison dataset, and generates a set of expression ratio values representing ratios of expression intensities in the selected and base expression datasets."

For example, Maslyn describes a comparison step that generates a set of expression ratio values representing ratios of expression intensities between the datasets. Applicants respectfully assert that the comparison of one dataset to another dataset is a process that produces a result that is a combination of the compared datasets such as the described set of expression ratio values. The comparison procedure that produces a combination result is different than the

claimed correlation result of each of the probe-set identifiers with gene or EST data because the result is not a combination of the probe-set identifiers and gene or EST data, but rather the gene or EST data itself is the result. Similarly, it is also different than a correlation of gene or EST data with protein data.

As the examiner points out in the office action mailed July 26, 2004 a definition of "correlate" includes:

> to establish a mutual or reciprocal relation between (Merriam-Webster online dictionary)

Thus, comparing two sets of data to generate a combined result does not establish a relation between the sets of data but rather is a processed combination of the two sets of data and therefore is not a correlation. Applicants also further assert that the comparison of the datasets described by Maslyn relates to the comparison of abundance data and does not result in a correlation with a set of protein data that is provided to a user.

Maslyn also describes optionally filtering dataset elements from the datasets employing a first filter (filter 533) and user defined query criteria, as described in col. 11, line 64 *et seq.* of Maslyn:

> "An optional filter 533 is provided. If the user had defined a set of query criteria, certain of these criteria are used to filter the dataset elements retrieved when the datasets are added to the working set in step 532. The filter criteria include filtering by abundance, transcript and/or by sequence using the blast query feature. However, the invention is not meant to be limited to the previous filter criteria, in an alternate embodiment, other filter criteria are used. The filter is enabled or disabled by the user."

Maslyn also describes a different, second filter (filter 540) for filtering elements of the datasets (col. 12, line 11 *et seq.*):

> "Another filter 540 allows a user to select specified elements of the dataset. The filter 540 includes a set of filtering tools, such as highlighting (selecting) and cropping.
>
> In step 542, the user selects one of the filtering functions or tools of the filter. The user can filter by abundance, abundance fold difference, abundance absolute difference, transcript absence, controls or protein function. However, the invention is not meant to be limited to the previous filtering functions, in an alternate embodiment, other filtering functions are used."

Applicants respectfully assert that the filters described by Maslyn and the correlation steps of the present invention are different. For example, Maslyn does not describe or suggest a filter that correlates probe-set identifiers with gene or EST data, where the gene or EST data is further correlated to protein data. Rather, Maslyn describes the output of the optional filter 533 and filter 540 as independently presented to the user (Figures 10A and 10B; and col. 12, line 39 *et seq.*).

For example, filter 540 does not employ the output from filter 533, and filter 533 does not employ the output from filter 540 for any correlation, comparison or similar operation where the inputs to each of filters 533 and 540 are independent of each other. Rather filter 540 and 533 each employs user defined query criteria and datasets as input for selection of specific elements. Thus, each of filter 540 and 533 employ independent inputs and produce independent outputs where Maslyn does not described or suggest that the output from one filter should be employed as the input to the other filter.

Further, the user defined query criteria as described by Maslyn are different than the claimed user selection of probe-set identifiers. For example, the query criteria as described by Maslyn refers to the act of filtering employing rules defined by the query criteria and does not refer to the data to be filtered. In contrast, the claimed user selection of probe-set identifiers represents the data to be acted upon and not the method of acting or rules to be applied by such a method.

The Examiner also asserts that Maslyn describes users selecting elements by their associated function that "represents" a correlation between gene data with protein domain information. The Examiner points to col. 14, lines 34-36 for support that states:

> "The viewer tools have a highlight by protein function menu option 668 that allows a user to select elements by their associated protein function."

Applicants respectfully assert that the viewer tool as described by Maslyn does not describe the claimed user selection of probe set identifiers based upon the results from one or more experiments and the multiple correlating steps. In particular, Maslyn does not describe or suggest two consecutive correlation steps such as the initial claimed step of a correlation of a user selection of probe-set identifiers with the gene or EST data and the correlation of gene or EST data with a set of protein data. Applicants also respectfully assert that Maslyn does not provide description or suggest combining the viewer tool with other elements or processes to produce the claimed combination. Therefore, Applicants respectfully

assert that the description of viewer tool does not describe the claimed invention either alone or in combination.

Therefore, Applicants respectfully assert that Maslyn does not teach the combination of elements of independent claims 19 and 49 are thus each patentable for the reasons given above. Also, each of claims 50-51, and 61-62, and 64-65 each depend from claims 19 or 49 and thus patentable for the same reasons.

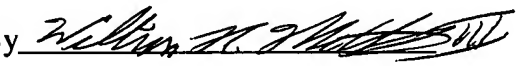
CONCLUSION

For these reasons, Applicants believe all pending claims are now in condition for allowance. If the Examiner has any questions pertaining to this application or feels that a telephone conference would in any way expedite the prosecution of the application, please do not hesitate to call the undersigned at (781) 280-1522.

The Commissioner is hereby authorized to charge any additional fees which may be required, or credit any overpayment to Deposit Account 01-0431.

Applicants respectfully request that a timely Notice of Allowance be issued in this case.

Respectfully submitted,

By 

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